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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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530	535.4	543.6	554.4	565.8	568.4	Score
93.0	93.9	95.4	97.3	99.3	99.7	Query Match
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ALIGNMENTS

RESULT 1
BG184448
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS JOURNAL MEDLINE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 807)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kiika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001) Athersys, Inc.
3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
Fax: 216 361 9596 Email: scain@athersys.com
High quality sequence stop:
Location/Qualifiers BG184448 807 bp mRNA linear EST 21-APR-RST3374 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence. BG184448 GI:13706135 Contact: Scott J. Cain Nat. Biotechnol. 21227151 Homo sapiens 499. НО 44115, USA Euteleostomi;
; Homo. EST 21-APR-2001

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AUTHORS
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/organism="Homo sapiens"
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/clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression',
Iibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

11 a 195 c 178 g 222 t 1 others
on, J.J., Sherf, B., Rundlett Leventhal, C., Thornton, M.,
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8.4e-151;
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193 c 173 g 214 t 1 others
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seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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The FAPESP/LICR Human Cancer Genome Project
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QV4-ST0212-120100-075-f09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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+55-11-2707001
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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Eukaryota; Metazoa; Chordata; ......

Mammalia; Eutheria; Primates; Catarrhini; Hominidae, .....

Mammalia; Eutheria; Primates; Catarrhini; Hominidae, .....

E 1 (bases 1 to 789)

S Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat Biotechnol. 19 (5), 440-445 (2001)
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3201 Carnegie Ave,
Tel: 216 431 9900
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Location/Qualifiers
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Athersys RAGE Library I
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
/notes using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
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Eukaryota; Metazoa; C
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1 (bases 1 to 837)
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                                    Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                              Nat. Bio
21227151
                   Contact: Scott
         Athersys, Inc
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Pred. No. 2.1e-141;
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quality sequence stop: '
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
/ibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                                                                                                                                     Contact: Scott J. Ca
Athersys, Inc.
3201 Carnegie Ave, (
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression.
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1 (bases 1 to 810)
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/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
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/db_xref="taxon:9606"
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Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Bitechnol. 19 (5), 440-445 (2001)
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216 361 9596
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
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Eutheria;
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97.28;
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                                                                                                                                                                                                                                                                               Score 523.6; DB 12;
Pred. No. 4.7e-138;
0; Mismatches 14;
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4st2=QV4-ST0212-
261199-045-c09st3=1999-11-26st4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 36.
Location/Qualifiers
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QV4-ST0212-261199-045-c09
BF375244
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
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               a
                                                            /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed low stringency conditions."

173 c 164 g 184 t
                                                                                                                                                /clone_lib="ST0212"
/dev_stage="Adult"
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Athersys,
3201 Carne
Tel: 216 4
Fax: 216 3
Email: sca
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 822)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression.
                                                                                                                                                                                                                             BG219307 822 bp mRNA linear RST39061 Athersys RAGE Library Homo sapiens cDNA, BG219307 BG219307.1 GI:13745328 EST.
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Eukaryota; M
                                                      Contact: Scott J. Cain
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         rsys, Inc.
Carnegie Ave, Cleveland,
216 431 9900
216 361 9596
                                                                             Biotechnol, 19
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93.4%;
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Pred. No. 3.4e-122;
0; Mismatches 32;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 871)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J,
Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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RST18188
BG198917
BG198917.
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a 169 c 179 g 230 t 3 others
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/cell_line="HT1080"
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/db_xref="taxon:9606"
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Pred. No. 8.5e-116;
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Contact: S
Athersys,
3201 Carne
Tel: 216 4
          Mus musculus (strain:C57BL/6J) adult male testis cDNA t clone_lib:RIKEN full-length enriched mouse cDNA library
                         HTC; CAP trapper.
Mus musculus (str
                                                              PLACE1009493, full
AK016573
                                                                                       Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932443L08:homolog to CDNA FLJ13593 FIS, CLONE
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lone:4932443L08.
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216 431 9900
216 361 9596
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
52 a 186 c 185 g 246 t 2 others
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22 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sogabe, Y., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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Hayashizaki,Y.
Direct Submission
Direct Submitsion
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (RIKEN), Laboratory for Genome Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC) PIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh
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                       ATCTTCTTGCTCTTTTTCCCCATCTTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC
                                                                               ATTTTCTTGCTCTTCCCATCCTTCACGGGAGTGCTGTGCACCCTGGCTATCACCATC
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                            678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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NFSFIIIPQFTVGAKNTLQFTGLEFFTGAGYFGDTVMYYGFYTNSTIRHRMGGASYNM
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2721
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2702. .2707
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                                                                                                                                                                                                                                                                                                                 , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smitl,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                    Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                  quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                scain@athersys.com
Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily
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                                                                  /note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                      Cleveland,
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                    BG982234
CM4-CN0089-130201-723-e04
BG982234
Email: asimpson@ludwig.org.br
This sequence was derived from t
Project. This entry can be seen
                                                         Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                       Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                            Eukaryota;
Mammalia; I
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                                                                                         Contact: Simpson A.J.G.
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GATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGA
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 594)
                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM4&t2=CM4-CN0089-
130201-723-e04&t3=2001-02-13&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CN0089"
/dev_stage="Adult"
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1. .447
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99.8%;
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Primates;
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                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                     bp mRNA linear EST 24-FEB sapiens cDNA clone IMAGE:2898861
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Search completed: November Job time: 2224 secs
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                                                                                                                                                           474 ATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAA 415
                                                                                                                                                                                                                                                                                                                                                                                                              529 TTGCGATCTAGAAGATCAGTTCAAGAAGGTAATCCAAGGGCC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAA 408
                                                                                  TTGCGATCTAGAAGATCAGTTCAAGAAGGTAATCCAAGGGCC
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 404.

Location/Qualifiers

1 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2898861"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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